

Figure 1

1 60
 SEQ ID NO:21 (gi 1709203) MARNGSLEEFGLGAVDAAKRAGEIIRKGFHETKHVVHKGQVDLVTTETDKACEDLI FNHLK
 SEQ ID NO:22 (gi 1709205) MAQNGSVEQFLDVAVEAAKAGEIIRREGFYKTKHVEHKGMDLVTTETDKACEDLI FNHLK
 SEQ ID NO:2 MAE-----EQFLAVDAAKNAGEIIRKGFYQTKNVEHKGQVDLVTTETDKACEDLI FNHLR
 SEQ ID NO:4 MVDNDSLSEFLASAVDAQKAGEIIRKGFYQTKNVEHKGQVDLVTTETDKACEELI FNHLK
 SEQ ID NO:6 MAE-----EQFLAAAVGAAKSAGEIIRKSFYLSKKVEHKGQVDLVTTETDKACEDLI FNHLR
 SEQ ID NO:8
 61 120
 SEQ ID NO:21 (gi 1709203) QHFPCHKFIGEETSAAT-GDFDLTDEPTWIIVDPVDGTTNFVHGFPFVCVSI GLTIGKIPT
 SEQ ID NO:22 (gi 1709205) QRFPSHKFIGEETAA-CGNFELTDEPTWIIVDPDLDGTTNFVHGFPFVCVSI GLTIEKKPT
 SEQ ID NO:2 KHYPDHKFIGEETSAGLATADLTDDPTWIIVDPDLDGTTNFVHGFPFVCVSI GLTVGK---
 SEQ ID NO:4 QLYPTHKFIGEETAA-YGTTELTDPTWIIVDPDLDGTTNFVHGFPFVCVSI GLTIGKTPT
 SEQ ID NO:6
 SEQ ID NO:8 MLYPDHKFIGEETSAALGSTDDLTDTWIIVDPDLDGTTNFVHGFPFVCVSI GLTIGKIPT
 121 180
 SEQ ID NO:21 (gi 1709203) VGVVYDPIIDELFTGINGKGAYLNGKPIKVSSQSELVKSLLGTEVGTTRDNLTVETTRR
 SEQ ID NO:22 (gi 1709205) VGVVYNPIIDELFTGIDKGAFNGKPIKVSSQSELVKALLATEAGTNRDKLVVDATTGR
 SEQ ID NO:2
 SEQ ID NO:4 IGVVYNPIINELFTGIHGKGAFLNGNPIKVSSQTELISSLATEAGTKR-----
 SEQ ID NO:6 VGVVYNPIMNELFTAVRGKGAFLNGSPIKTSQNELVKALMVTEVGTKRDKSTLDDTTNR
 SEQ ID NO:8
 181 240
 SEQ ID NO:21 (gi 1709203) INNLLEKVRSLRMCGSCALDLGWACGRLEFLYIGYGGPWDVAGGAVIVKEAGGVLFDP
 SEQ ID NO:22 (gi 1709205) INSLLEKVRSLRMCGSCALNLCGVACGRDLDFELEFGGPDVAGGAVIVKEAGGVFDP
 SEQ ID NO:2
 SEQ ID NO:4
 SEQ ID NO:6
 SEQ ID NO:8 INKLLFKIRSI RMCGSLALNMGVACGRDLICYEIGFGGPDVAGGAVIVKEAGGVFDP
 241 277
 SEQ ID NO:21 (gi 1709203) SGSEFDITSQRVAATNPHLKEAFVEA---LQLSEYVS
 SEQ ID NO:22 (gi 1709205) SGSEFDLTARRVAATNAHLKDAFIKA---LNE-----I
 SEQ ID NO:2
 SEQ ID NO:4
 SEQ ID NO:6 SGADFAITSQRVAVSNPFXXKDELVETRRKMGWEIYN.
 SEQ ID NO:8 SGDEFDLMAQRMAGSNGHLKDQFIKA---LGDAS.---

Figure 2

SEQ ID NO:23	(gi 3915048)	M-----TSAQKPVF-----SPSDLQT-----WL-----	60
SEQ ID NO:24	(gi 1652942)	ML-----PEVEQRLF-----	
SEQ ID NO:10		-----	
SEQ ID NO:12		-----	
SEQ ID NO:14		MLSSSSSTHSDTSPFPGGLASANPNRSLRLRLRAASPVSSAVLSASGRQP-----MSTV	
SEQ ID NO:16		-----	
SEQ ID NO:18		MFSQCH-----FLSHSPIPNTT-FRLRAMAPHST-----	
SEQ ID NO:20		-----HETKPSLP-----YHLRSPSLLATFSSSAAGRACGIAGRWMGVS	
1			
SEQ ID NO:23	(gi 3915048)	-----EIA TEAVLAAGAEI--FSLWGKVQIQIEKGRAG	120
SEQ ID NO:24	(gi 1652942)	-----IAQQLAAVSGEILLIQYFRRSHLQGGTKIDQVS	
SEQ ID NO:10		-----	
SEQ ID NO:12		-----	
SEQ ID NO:14		RASFAAGAAGRRAAAVGE--LATERLVEVAQRAADAAGEVLRKYFRQ-RVEIIDKEDHSP	
SEQ ID NO:16		-----	
SEQ ID NO:18		-----PLELNRF AEVGNKVADAAGEVIRKYFRK-NFDVIHKHDLSP	
SEQ ID NO:20		RAS-PSEAGGWAVAAAGKEGVDMERLVAVAQSAADAAGEVLRKYFRQ-RFEIIDKEDHSP	
61			
SEQ ID NO:23	(gi 3915048)	-----	
SEQ ID NO:24	(gi 1652942)	-----	
SEQ ID NO:10		-----	
SEQ ID NO:12		-----	
SEQ ID NO:14		-----	
SEQ ID NO:16		-----	
SEQ ID NO:18		-----	
SEQ ID NO:20		-----	
121			
SEQ ID NO:23	(gi 3915048)	DLVTEADRQAEAIILEI IKRRCPDHAILAEESG-QLGQVDNPF CWAIDPLDGTTFNFAHSY	180
SEQ ID NO:24	(gi 1652942)	AIVTQADEEAEQAMVDLIQAQFPQDGVIREEG--KNIAGKSGYTWLDPIDGTSSEFVRGL	
SEQ ID NO:10		-----HEDKLSSEVILEVWTKNFRDHLILGEEGG-LIGDSLSEYLCIDPLDGTTFNFAHGY	
SEQ ID NO:12		-----	
SEQ ID NO:14		--VTIADREAEEMVSVILKSFPTHAIFGEENGWRC AENSADFVWVLDPIDGTSKFITGK	
SEQ ID NO:16		-----HE-----	
SEQ ID NO:18		--VTIADQSAEEAMVSIILDNFP SHAIYGEENGWRC EKNADYVWVLDPIDGTSKFITGK	
SEQ ID NO:20		--VTIADREAEEMTSVILKSFPTHAVFGEENGWRC AEKSADYVWVLDPIDGTSKFITGK	

SEQ ID NO:23	(gi 3915048)	181	PVSCVSIQLLIQDIPTVGVVYNPFROELFRAATSLGATLNR-----RPIQVSTTASLDK	240
SEQ ID NO:24	(gi 1652942)		PIFATLIGLVADMRPVLGIAHQPISGDRWQGVQGEQSNVNGIP-LVNPYKASEINLTAA	
SEQ ID NO:10			PSFSVSIQVLRGKPAATVVEFCGGPMCWSTRTISASSKGAYCNGQKIHVSPTEKVEQ	
SEQ ID NO:12			-----MCWTTRTIFPFAGGGAYIGQRIHVSQTDKVEQ	
SEQ ID NO:14			PLFGTLIALHNG-KPVIQVIDQPILRERWIGVDGKQTTLNGQE-I--SVRSCNL-LAQ	
SEQ ID NO:16			-----LTKVEQ	
SEQ ID NO:18			PVFGTLVALLQNG--TPILGIIDQVLRERWIGIAGKRTSLNGQE-I--STRTCAD-LSQA	
SEQ ID NO:20			PLFGTLIALHNG-KPVMGIIDQVLRERWVGVDGKKTTLNGQE-I--SVRPCNV-LEQA	
SEQ ID NO:23	(gi 3915048)	241	SLLVTG---FAYDRVKTLDNNYFECYLTHTLQGVRRSGSAIDLIDVACGRLDGYWERG	300
SEQ ID NO:24	(gi 1652942)		CIVSTTPLMFTTPVQQQKMAIYRQCQRTAFGGDCFNLSAASGWTAMPLVIVEA----D	
SEQ ID NO:10			SLLVTG---FGYHDDAWLTNINLFKEFTDVRGVRRLGSAADMVSHVGLGITEAYWEYR	
SEQ ID NO:12			SLLVTGFGYEHDDAWTNNLNFKEFTDISRGVRR--LGSAAADMVSHVGLGITEAYWE	
SEQ ID NO:14			YLYTTSPLHFEADAEDA-FIRVRNKVPLYGCDYAYALLASGFVDI---VVES-----G	
SEQ ID NO:16			SLLVTG---FGYHDDAWVTNINLFKEYTDISRGVRRRLGSAADMVSHVGLGITEAYWEYR	
SEQ ID NO:18			YLYTTSPLHFNDAEEA-FIRVRKVKFQLYGCDYAYALLSSGFVDL---VVES-----G	
SEQ ID NO:20			YLYTTSPLHFEADAEDA-FIRVRDKVKPLYGCDYAYALLASGFVDL---VVES-----G	
SEQ ID NO:23	(gi 3915048)	301	INPMDAAGIVIVREAGGIVSAYDCSPLDLSTGRILATNGKIHQELSQAALATPQ-----	360
SEQ ID NO:24	(gi 1652942)		LNFYDFCALIPILTCANYCFTDWQKEL-----TPESTEVVASPNPKLHSE	
SEQ ID NO:10			LKPWMDAAGVLIVEEAGGVVTRMDGGGFTVDRSVLVSNVGVHDQLLERIRPATEDLKKK	
SEQ ID NO:12			YRLKPWDVHAGVLIVEEAGGVVTRMDGGGFTVDRSVLVSNGLVHGQV-----	
SEQ ID NO:14			LKPYDFLSLVPVIEGAGGSITDWRGDKLH-----WPVTAESRPTSFNVVAAGDARVHKE	
SEQ ID NO:16			LKPWMDAAGVLIVEEAGGMVSRMDGGGFTVDRSVLVSNVGVHDQLLDRIGPATEDLKKK	
SEQ ID NO:18			LKPYDFLALIPVIEGAGGVITDWGDKLF-----WEASPLSIATSFNVVAAGDKQIHQQ	
SEQ ID NO:20			LKPYDFLSLVPVIEGAGGSITDWEGNKLH-----WPVSSESERPTSFNVVAAGDSHVHGQ	
SEQ ID NO:23	(gi 3915048)	361	-----WF--QYAAARAQKI	381
SEQ ID NO:24	(gi 1652942)		ILAFI---Q-----	
SEQ ID NO:10			GIDFSLWFKPKDYPT---DF.	
SEQ ID NO:12			-----CL	
SEQ ID NO:14			ALDALRWR.-----	
SEQ ID NO:16			GIDFSLWFKPKDYPT---DF.	
SEQ ID NO:18			ALDSLQWK.-----	
SEQ ID NO:20			ALALRWR.-----	